

# Simon Gravel

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

7,089  
citations

279798  
23  
h-index

315739  
38  
g-index

61  
all docs

61  
docs citations

61  
times ranked

13049  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. Science, 2012, 337, 64-69.	12.6	1,535
2	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. American Journal of Human Genetics, 2017, 100, 635-649.	6.2	1,120
3	RFMix: A Discriminative Modeling Approach for Rapid and Robust Local-Ancestry Inference. American Journal of Human Genetics, 2013, 93, 278-288.	6.2	686
4	Demographic history and rare allele sharing among human populations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11983-11988.	7.1	589
5	Reconstructing the Population Genetic History of the Caribbean. PLoS Genetics, 2013, 9, e1003925.	3.5	296
6	Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. American Journal of Human Genetics, 2013, 93, 852-864.	6.2	284
7	Population Genetics Models of Local Ancestry. Genetics, 2012, 191, 607-619.	2.9	272
8	Estimating the mutation load in human genomes. Nature Reviews Genetics, 2015, 16, 333-343.	16.3	233
9	Genomic Insights into the Ancestry and Demographic History of South America. PLoS Genetics, 2015, 11, e1005602.	3.5	198
10	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. PLoS Genetics, 2013, 9, e1004023.	3.5	185
11	Inferring the Joint Demographic History of Multiple Populations: Beyond the Diffusion Approximation. Genetics, 2017, 206, 1549-1567.	2.9	176
12	The Great Migration and African-American Genomic Diversity. PLoS Genetics, 2016, 12, e1006059.	3.5	166
13	UMAP reveals cryptic population structure and phenotype heterogeneity in large genomic cohorts. PLoS Genetics, 2019, 15, e1008432.	3.5	166
14	Efficient ancestry and mutation simulation with msprime 1.0. Genetics, 2022, 220, .	2.9	133
15	Computationally Efficient Composite Likelihood Statistics for Demographic Inference. Molecular Biology and Evolution, 2016, 33, 591-593.	8.9	112
16	A community-maintained standard library of population genetic models. ELife, 2020, 9, .	6.0	112
17	The impact of agricultural emergence on the genetic history of African rainforest hunter-gatherers and agriculturalists. Nature Communications, 2014, 5, 3163.	12.8	96
18	Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3596-603.	7.1	91

#	ARTICLE	IF	CITATIONS
19	When Is Selection Effective?. Genetics, 2016, 203, 451-462.	2.9	73
20	A review of UMAP in population genetics. Journal of Human Genetics, 2021, 66, 85-91.	2.3	73
21	Spatially mapping the immune landscape of melanoma using imaging mass cytometry. Science Immunology, 2022, 7, eabi5072.	11.9	60
22	Models of archaic admixture and recent history from two-locus statistics. PLoS Genetics, 2019, 15, e1008204.	3.5	57
23	Dense Periodic Packings of Tetrahedra with Small Repeating Units. Discrete and Computational Geometry, 2010, 44, 245-252.	0.6	47
24	Accounting for long-range correlations in genome-wide simulations of large cohorts. PLoS Genetics, 2020, 16, e1008619.	3.5	43
25	Unbiased Estimation of Linkage Disequilibrium from Unphased Data. Molecular Biology and Evolution, 2020, 37, 923-932.	8.9	26
26	Genomic inference using diffusion models and the allele frequency spectrum. Current Opinion in Genetics and Development, 2018, 53, 140-147.	3.3	25
27	Legacy Data Confound Genomics Studies. Molecular Biology and Evolution, 2020, 37, 2-10.	8.9	23
28	Lessons Learned from Bugs in Models of Human History. American Journal of Human Genetics, 2020, 107, 583-588.	6.2	23
29	The existence and abundance of ghost ancestors in biparental populations. Theoretical Population Biology, 2015, 101, 47-53.	1.1	21
30	On the decidability of population size histories from finite allele frequency spectra. Theoretical Population Biology, 2018, 120, 42-51.	1.1	16
31	Intratumor Heterogeneity and Circulating Tumor Cell Clusters. Molecular Biology and Evolution, 2018, 35, 2135-2144.	8.9	16
32	Upper Bound on the Packing Density of Regular Tetrahedra and Octahedra. Discrete and Computational Geometry, 2011, 46, 799-818.	0.6	15
33	Recent shifts in the genomic ancestry of Mexican Americans may alter the genetic architecture of biomedical traits. ELife, 2020, 9, .	6.0	15
34	Predicting Discovery Rates of Genomic Features. Genetics, 2014, 197, 601-610.	2.9	14
35	Inferring Transmission Histories of Rare Alleles in Population-Scale Genealogies. American Journal of Human Genetics, 2018, 103, 893-906.	6.2	13
36	Assumptions about frequency-dependent architectures of complex traits bias measures of functional enrichment. Genetic Epidemiology, 2021, 45, 621-632.	1.3	5

#	ARTICLE	IF	CITATIONS
37	The Genetic and Molecular Analyses of RAD51C and RAD51D Identifies Rare Variants Implicated in Hereditary Ovarian Cancer from a Genetically Unique Population. Cancers, 2022, 14, 2251.	3.7	4
38	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
39	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
40	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
41	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
42	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
43	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0